

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga  
Au-Young, Janice  
Goli, Surya K.  
Hillman, Jennifer.  
Zweiger, Gary B.

(ii) TITLE OF THE INVENTION: A NOVEL TUMOR PROTEIN

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: U.S.  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0126 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:  
(B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Ala Gin Ala Gln Gly Leu Leu Glu Thr Glu Pro Leu Gln Gly  
 1 5 10 15  
 Thr Asp Glu Asp Ala Val Ala Ser Ala Asp Phe Ser Ser Met Leu Ser  
 20 25 30  
 Glu Glu Glu Lys Glu Glu Leu Lys Ala Glu Leu Val Gln Leu Glu Asp  
 35 40 45  
 Glu Ile Thr Thr Leu Arg Gln Val Leu Ser Ala Lys Glu Arg His Leu  
 50 55 60  
 Val Glu Ile Lys Gln Lys Leu Gly Met Asn Leu Met Asn Glu Leu Lys  
 65 70 75 80  
 Gln Asn Phe Ser Lys Ser Trp His Asp Met Gln Thr Thr Ala Tyr  
 85 90 95  
 Lys Lys Thr His Glu Thr Leu Ser His Ala Gly Gln Lys Ala Thr Ala  
 100 105 110  
 Ala Phe Ser Asn Val Gly Thr Ala Ile Ser Lys Lys Phe Gly Asp Met  
 115 120 125  
 Ser Tyr Ser Ile Arg His Ser Ile Ser Met Pro Ala Met Arg Asn Ser  
 130 135 140  
 Pro Thr Phe Lys Ser Phe Glu Glu Arg Val Glu Thr Thr Val Thr Ser  
 145 150 155 160  
 Leu Lys Thr Lys Val Gly Gly Thr Asn Pro Asn Gly Gly Ser Phe Glu  
 165 170 175  
 Glu Val Leu Ser Ser Thr Ala His Ala Ser Ala Gln Ser Leu Ala Gly  
 180 185 190  
 Gly Ser Arg Arg Thr Lys Glu Glu Glu Leu Gln Cys  
 195 200

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCCAGCTG	CGTTCTGAGC	CTGGGCGCAG	CTACCATCTG	CTCTGGGAAG	CACCAGGGTG	60
TCCCCGCGC	CCTCAGCTG	AAGTCAGCCA	CCATGGAGGC	GCAGGGACAA	GGTTTGTG	120
AGACTGAACC	GGTGCAGGAA	ACAGACGAAG	ATGCAGTAGC	CAGTGCCTGAC	TTCTCTAGCA	180
TGCTCTCTGA	GGAGGAAAAG	GAAGAGTTAA	AAGCAGAGTT	AGTTCACTGA	GAAGACGAAA	240
TTACAACACT	ACGACAAGTT	TTGTCAGCGA	AAGAAAGGCA	TCTAGTTGAG	ATAAAACAAA	300
AACTCGGCAT	GAACCTGATG	AATGAATTAA	AACAGAACTT	CAGCAAAAGC	TGGCATGACA	360
TGCAGACTAC	CACTGCCCTAC	AAGAAAACAC	ATGAAAACCT	GAGTCACGCA	GGGCAAAAGG	420
CAACTGCAGC	TTTCAGCAAC	GTTGGAACGG	CCATCAGCAA	GAAGTTCGGA	GACATGAGTT	480
ACTCCATTCG	CCATTCCATA	AGTATGCCCTG	CTATGAGGAA	TTCTCCTACT	TTCAAATCAT	540
TTGAGGAGAG	GGTTGAGACA	ACTGTCACAA	GCCTCAAGAC	GAAAGTAGGC	GGTACGAAACC	600
CTAATGGAGG	CAGTTTGAG	GAGGTCTCA	GCTCCACGGC	CCATGCCAGT	GCCCAGAGCT	660
TGGCAGGAGG	CTCCCGGCGG	ACCAAGGAGG	AGGAGCTGCA	GTGCTAAGTC	CAGCCAGCGT	720

GCAGTGCATC CAGAAACCGG CCACTACCCA GCCCATCTNT GCCTGTGCTT ATCCAGATAA 780  
 GAAGACCAAA 790

## (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY:  
 (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro  
 1 5 10 15  
 Tyr Phe Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe  
 20 25 30  
 Trp Lys Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys  
 35 40 45  
 Lys Met Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile  
 50 55 60  
 Tyr Asp Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp  
 65 70 75 80  
 Leu Ile Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu  
 85 90 95  
 Tyr Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile  
 100 105 110  
 Met Ser Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe  
 115 120 125  
 Asp Trp Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val  
 130 135 140  
 His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp  
 145 150 155 160  
 Leu Tyr His Asn Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser  
 165 170 175  
 Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu  
 180 185 190  
 Gly Ser Trp Ala Arg Leu Asp Ala Arg Ala Val Val Thr Gly Leu Leu  
 195 200 205  
 Ala Leu Lys His Phe Gly Pro Val Cys Arg Arg Cys Gln Cys Ala Leu  
 210 215 220  
 Leu Gly Leu Val Ser Gln Thr Leu Met Tyr Leu Phe Pro Ala Ser Leu  
 225 230 235 240  
 Gln Val Leu Val Lys  
 245

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 888 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- .. (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY:
  - (B) CLONE: Consensus

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTMGMKCGCG	GGCCCCCGCC	AGTCAGGTGG	GTGCCAGGCC	CTGGCCGTGG	CGAAAGAGCC	60
GGCGGAGGGA	GGACCCGCTC	CCGGAGACGC	CGCCTCGCGA	TCCCCGCGCG	GGCGGGACCG	120
GGCGGCCGGC	ATCATGACCC	TGTTTCACTT	CGGGAACCTGC	TTCGCTCTTG	CCTACTTCCC	180
CTACTTCATC	ACCTACAAGT	GCAGCGGCCT	GTCCGAGTAC	AACGCCCTCT	GGAAATGCGT	240
CCAGGCTGGA	GTCAACCTACC	TCTTTGTCCA	ACTCTGCAAG	ATGCTGTTCT	TGGCCACTTT	300
CTTTCCCAACC	TGGGAAGGCG	GCATCTATGA	CTTCATGGG	GAGTCATGA	AGGCCAGCGT	360
GGATGTGGCA	GACCTGTAG	GTCTAACCT	TGTATGTCC	CGGAATGCCG	GCAAGGGAGA	420
GTACAAGATC	ATGGTTGCTG	CCCTGGGCTG	GGCCACTGTC	GAGCTTATT	TGTCCCCTG	480
CATTCCCTA	TGGGTGCGAG	CCCGGGCAT	TGAGTTGAC	TGGAAGTACA	TCCAGATGAG	540
CATAGACTCC	AAACATCAGTC	TGGTCATTA	CATCGTCGCG	TCTGCTCAGG	TCTGGATGAT	600
AAACACGCTAT	GATCTGTACC	ACAACCTCCG	GGCAGCTGTC	CTTCTGCTGA	TGTTCCCTCAG	660
TGTCTACAAG	GCCTTTGTTA	TGGAGACCTT	CGTCCACCTC	TGCTCGCTGG	GCAGTTGGC	720
ARCTCTAMT	GCCCGAGCAG	TGGTAACGGG	GCTGCTGGCC	CTCAAGCACT	TTGGSCCTGT	780
ATGTCGSCGT	TGTCAATGTG	CACTYCTAGG	CTTGGTGTCT	CAGACATTGA	TGTACCTTT	840
CCCTGCCTCA	CTCCAGGTTT	TAGTGAAGTA	AAACAGTATT	GGAAAGTT		888

- (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 184 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: GenBank
  - (B) CLONE: 790225

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	Arg	Gly	Glu	Gln	Gly	Leu	Leu	Arg	Thr	Asp	Pro	Val	Pro	Glu
1															15
Glu	Gly	Glu	Asp	Val	Ala	Ala	Thr	Ile	Ser	Ala	Thr	Glu	Thr	Leu	Ser
															30
Glu	Glu	Glu	Gln	Glu	Glu	Leu	Arg	Arg	Glu	Leu	Ala	Lys	Val	Glu	Glu
															45
Glu	Ile	Gln	Thr	Leu	Ser	Gln	Val	Leu	Ala	Ala	Lys	Glu	Lys	His	Leu
															60
Ala	Glu	Ile	Lys	Arg	Lys	Leu	Gly	Ile	Asn	Ser	Leu	Gln	Glu	Leu	Lys
															80
Gln	Asn	Ile	Ala	Lys	Gly	Trp	Gln	Asp	Val	Thr	Ala	Thr	Ser	Ala	Tyr
															95
Lys	Lys	Thr	Ser	Glu	Thr	Leu	Ser	Gln	Ala	Gly	Gln	Lys	Ala	Ser	Ala
															110
100															
105															

AB

Ala Phe Ser Ser Val Gly Ser Val Ile Thr Lys Lys Leu Glu Asp Val  
 115 120 125  
 Lys Asn Ser Pro Thr Phe Lys Ser Phe Glu Glu Lys Val Glu Asn Leu  
 130 135 140  
 Lys Ser Lys Val Gly Gly Thr Lys Pro Ala Gly Gly Asp Phe Gly Glu  
 145 150 155 160  
 Val Leu Asn Ser Ala Ala Asn Ala Ser Ala Thr Thr Thr Glu Pro Leu  
 165 170 175  
 Pro Glu Lys Thr Gln Glu Ser Leu  
 180

## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1072344

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Pro Lys Gly Asn Lys Pro Asn Glu Lys Lys Glu Glu Leu Glu  
 1 5 10 15  
 Lys Phe Ala Lys Glu Leu Gln Gly Ser Asp Ser Asp Glu Asp Ala Val  
 20 25 30  
 Val Ile Glu Gln Pro Thr Val Glu Pro Lys Leu Pro Gln Asn Asp Ser  
 35 40 45  
 Ser Ser Ser Asn Lys Ile Val Leu Ser Gln Ala Glu Lys Asp Leu Leu  
 50 55 60  
 Arg Thr Glu Leu Asp Lys Thr Glu Glu Glu Ile Ser Thr Leu Lys Gln  
 65 70 75 80  
 Val Leu Ser Ala Arg Gln Lys His Ala Ala Glu Leu Lys Arg Lys Leu  
 85 90 95  
 Gly Leu Thr Pro Phe Ser Glu Leu Ser Gln Asp Ile Asn Arg Ser Leu  
 100 105 110  
 Lys Thr Val Thr Asp Thr Asp Ala Cys Thr His Phe Ile Glu Ile Asn  
 115 120 125  
 Ile Gln Lys Lys Lys Gln Ser Met Tyr Tyr Ile Lys Arg Leu Ser  
 130 135 140  
 Lys Asn Ile Gln Thr Val Pro Ile Leu Thr Ser Glu Lys Lys Arg Ile  
 145 150 155 160  
 Leu His Ala Phe Ile Val Leu Lys Lys Lys Ser Ser Ile Leu Lys Ser  
 165 170 175  
 Leu Leu Leu Trp Gln Gln Tyr Gln Lys Thr Ala Glu Val Ala Ala  
 180 185 190  
 Thr Ser Asp Thr Val Lys Glu Lys Trp Asn Asp Met Arg Asn Ser Ser  
 195 200 205  
 Leu Phe Lys Ser Phe Glu Ser Lys Leu Gly Ser Ala Leu Asn Asn Ala  
 210 215 220  
 Lys Met Ala Ala Ser Thr Ser Ile Asp His Leu Ala Gly Ala Ala Arg  
 225 230 235 240

Gly Pro Ser Gln Thr Gly Thr Pro Val Ala Glu Glu Ala Lys Pro Ile  
 245 250 255  
 Ser

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 470373

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Phe Phe His Phe Ile Asn Cys Phe Ala Leu Ala Phe Ala Pro  
 1 5 10 15  
 Tyr Phe Ile Val Tyr Lys Tyr Ser Gly Ile Asn Glu Tyr Ser Ser Ile  
 20 25 30  
 Trp Lys Cys Ala Thr Ala Ser Gly Gly Tyr Leu Leu Thr Gln Leu Ala  
 35 40 45  
 Lys Leu Leu Ile Ile Ala Thr Phe Phe Pro Ala Leu Asp Ser Glu Gly  
 50 55 60  
 Phe Ser Ile Val Pro Glu Phe Leu Lys Ser Ser Ala Asp Ile Ile Asp  
 65 70 75 80  
 Val Ile Gly Leu His Leu Leu Met Thr Asn Phe Leu Ala Gly Lys Gly  
 85 90 95  
 Glu Val Arg Phe Val Val Gly Gly Leu Gly Trp Gly Phe Ala His Ser  
 100 105 110  
 Val Ala His Arg Leu Val Leu Leu Trp Val Gly Ala Arg Gly Thr Ala  
 115 120 125  
 Phe Thr Trp Arg Trp Val Gln Thr Ser Leu Asp Ser Ser Ala Asp Leu  
 130 135 140  
 Leu Val Ile Val Ser Leu Ala Cys Leu Thr Trp Met Ile Thr Arg Thr  
 145 150 155 160  
 Pro Asn Lys Phe Leu Val Ser Pro Ile Leu Ala Ile Thr Val Gln His  
 165 170 175  
 Thr Phe Ser Leu Tyr Gly Trp Ser Leu Leu Ala Phe Arg Phe Ala Tyr  
 180 185 190  
 Ser Ile Ala Thr Ala Ile Leu Thr Val Val Val Tyr Ser Ala Asn Arg  
 195 200 205  
 Thr Ala Ser Thr Arg Lys Asn Glu  
 210 215